

MAY 08 2002

0907260 #50802

1

SEQUENCE LISTING

<110> ULLRICH, AXEL
GISHIZKY, MIKHAIL
SURES, IRMINGARD

<120> NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES

<130> 038602/1260

<140> 09/977,260

<141> 2001-10-16

<150> 08/232,545

<151> 1994-04-22

<160> 24

<170> PatentIn Ver. 2.1

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<211> 2000

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<222> (258)..(1778)

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tttccctctg gggggcg atg gcg ggg cga ggc tct ctg gtt tcc tgg cgg      290
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His Thr Ser Gly Gln Glu Gly Leu Leu Ala Ala Gly Ala Leu Arg Glu	
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Arg Glu Ala Leu Ser Ala Asp Pro Lys Leu Ser Leu Met Pro Trp Phe	
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His Gly Lys Ile Ser Gly Gln Glu Ala Val Gln Gln Leu Gln Pro Pro	
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Thr Leu Gly Ala Gln Ile Gly Glu Gly Glu Phe Gly Ala Val Leu Gln	
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Val Thr Ala Gln Ala Phe Leu Asp Glu Thr Ala Val Met Thr Lys Met	
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Gly Leu Asp Ser Ser Arg Leu Pro Val Lys Trp Thr Ala Pro Glu Ala	
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Cys Trp Glu Ala Glu Pro Ala Arg Arg Pro Pro Phe Arg Lys Leu Ala	
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Trp	His	Pro	Pro	Pro	Val	Ser	Ala	Arg	Met	Pro	Thr	Arg	Arg	Trp	Ala
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Pro	Gly	Thr	Gln	Cys	Ile	Thr	Lys	Cys	Glu	His	Thr	Arg	Pro	Lys	Pro
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Cys	Glu	Asn	Lys	Ser	Trp	Tyr	Arg	Val	Lys	His	His	Thr	Ser	Gly	Gln
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Glu	Gly	Leu	Leu	Ala	Ala	Gly	Ala	Leu	Arg	Glu	Arg	Glu	Ala	Leu	Ser
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Ser	Phe	Gly	Arg	Asp	Val	Ile	His	Tyr	Arg	Val	Leu	His	Arg	Asp	Gly
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 Gln Lys Val Ala Val Lys Asn Ile Lys Cys Asp Val Thr Ala Gln Ala
 260 265 270
 Phe Leu Asp Glu Thr Ala Val Met Thr Lys Met Gln His Glu Asn Leu
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 Glu His Val Ser Lys Gly Asn Leu Val Asn Phe Leu Arg Thr Arg Gly
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 Arg Ala Leu Val Asn Thr Ala Gln Leu Leu Gln Phe Ser Leu His Val
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 Ala Glu Gly Met Glu Tyr Leu Glu Ser Lys Lys Leu Val His Arg Asp
 340 345 350
 Leu Ala Ala Arg Asn Ile Leu Val Ser Glu Asp Leu Val Ala Lys Val
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 Ser Asp Phe Gly Leu Ala Lys Ala Glu Arg Lys Gly Leu Asp Ser Ser
 370 375 380
 Arg Leu Pro Val Lys Trp Thr Ala Pro Glu Ala Leu Lys His Gly Lys
 385 390 395 400
 Phe Thr Ser Lys Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu
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 Cys Pro Gly Pro Val His Val Leu Met Ser Ser Cys Trp Glu Ala Glu
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 Pro Ala Arg Arg Pro Pro Phe Arg Lys Leu Ala Glu Lys Leu Ala Arg
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aaa gaa cgg ctt ttt gtt ttg acc aaa aca aac ctt tcc tac tat gaa 207
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tat gac aaa atg aaa agg ggc agc aga aaa gga tcc att gaa att aag 255
Tyr Asp Lys Met Lys Arg Gly Ser Arg Lys Gly Ser Ile Glu Ile Lys
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Val Tyr Ala Ser Asn Glu Glu Ser Arg Ser Gln Trp Leu Lys Ala Leu
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caa aaa gag ata agg ggt aac ccc cac ctg ctg gtc aag tac cat agt 447
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gca gcc cca gga tgt acc ctc tgg gaa gca tat gct aat ctg cat act 543
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Asn Ser Lys Lys Ile Tyr Gly Ser Gln Pro Asn Phe Asn Met Gln Tyr	
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Glu Asn Tyr Cys Phe Asp Ser Ile Pro Lys Leu Ile His Tyr His Gln	
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<223> Description of Unknown Organism: Megakaryocyte
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Gly Ser Arg Lys Gly Ser Ile Glu Ile Lys Lys Ile Arg Cys Val Glu
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Lys Val Asn Leu Glu Glu Gln Thr Pro Val Glu Arg Gln Tyr Pro Phe
 65 70 75 80

Gln Ile Val Tyr Lys Asp Gly Leu Leu Tyr Val Tyr Ala Ser Asn Glu
 85 90 95

Glu Ser Arg Ser Gln Trp Leu Lys Ala Leu Gln Lys Glu Ile Arg Gly
 100 105 110
 Asn Pro His Leu Leu Val Lys Tyr His Ser Gly Phe Phe Val Asp Gly
 115 120 125
 Lys Phe Leu Cys Cys Gln Gln Ser Cys Lys Ala Ala Pro Gly Cys Thr
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 145 150 155 160
 His Arg Val Pro Thr Phe Pro Asp Arg Val Leu Lys Ile Pro Arg Ala
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 195 200 205
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 260 265 270
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 Val Arg Asn Ser Ser Gln Val Gly Met Tyr Thr Val Ser Leu Phe Ser
 325 330 335
 Lys Ala Val Asn Asp Lys Lys Gly Thr Val Lys His Tyr His Val His
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 Thr Asn Ala Glu Asn Lys Leu Tyr Leu Ala Glu Asn Tyr Cys Phe Asp
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 Ser Ile Pro Lys Leu Ile His Tyr His Gln His Asn Ser Ala Gly Met
 370 375 380
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 385 390 395 400

11

Asp Ser Val Ser Leu Gly Asn Gly Ile Trp Glu Leu Lys Arg Glu Glu
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 Ile Thr Leu Leu Lys Glu Leu Gly Ser Gly Gln Phe Gly Val Val Gln
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 Met Lys Leu Ser His Pro Lys Leu Val Lys Phe Tyr Gly Val Cys Ser
 465 470 475 480
 Lys Glu Tyr Pro Ile Tyr Ile Val Thr Glu Tyr Ile Ser Asn Gly Cys
 485 490 495
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 Val Leu Asp Asp Gln Tyr Val Ser Ser Val Gly Thr Lys Phe Pro Val
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 Lys Trp Ser Ala Pro Glu Val Phe His Tyr Phe Lys Tyr Ser Ser Lys
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 Gly Lys Gln Pro Tyr Asp Leu Tyr Asp Asn Ser Gln Val Val Leu Lys
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<223> Description of Unknown Organism: Megakaryocyte
kinase 3

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agctcctgct cagttttgcc tcggggtagc acctccagcc acagaaagca agccggtaag 180
tctctccagg taggacttgc tgcaaccacg ctgctggact gatctgaaac gggactttgc 240
atactctccg aagtatgggtg agttgggtgct gacttcaaag ttgcctgggtg aaggaagata 300
aggtggatcg cagagactaa ggggagaggg agaagccctg ctctctttct cccaccaag 360
gcaca atg agc aac atc tgt cag agg ctc tgg gag tac cta gaa ccc tat 410
      Met Ser Asn Ile Cys Gln Arg Leu Trp Glu Tyr Leu Glu Pro Tyr
        1             5             10             15

ctc ccc tgt ttg tcc acg gag gca gac aag tca acc gtg att gaa aat 458
Leu Pro Cys Leu Ser Thr Glu Ala Asp Lys Ser Thr Val Ile Glu Asn
              20             25             30

cca ggg gcc ctt tgc tct ccc cag tca cag agg cat ggc cac tac ttt 506
Pro Gly Ala Leu Cys Ser Pro Gln Ser Gln Arg His Gly His Tyr Phe
              35             40             45

gtg gct ttg ttt gat tac cag gct cgg act gct gag gac ttg agc ttc 554
Val Ala Leu Phe Asp Tyr Gln Ala Arg Thr Ala Glu Asp Leu Ser Phe
              50             55             60

cga gca ggt gac aaa ctt caa gtt ctg gac act ttg cat gag ggc tgg 602
Arg Ala Gly Asp Lys Leu Gln Val Leu Asp Thr Leu His Glu Gly Trp
              65             70             75

tgg ttt gcc aga cac ttg gag aaa aga cga gat ggc tcc agt cag caa 650
Trp Phe Ala Arg His Leu Glu Lys Arg Arg Asp Gly Ser Ser Gln Gln
              80             85             90

cta caa ggc tat att cct tct aac tac gtg gct gag gac aga agc cta 698
Leu Gln Gly Tyr Ile Pro Ser Asn Tyr Val Ala Glu Asp Arg Ser Leu
              100            105            110

cag gca gag ccg tgg ttc ttt gga gca atc gga aga tca gat gca gag 746
Gln Ala Glu Pro Trp Phe Phe Gly Ala Ile Gly Arg Ser Asp Ala Glu
              115            120            125

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aaa caa cta tta tat tca gaa aac aag acc ggt tcc ttt cta atc aga	794
Lys Gln Leu Leu Tyr Ser Glu Asn Lys Thr Gly Ser Phe Leu Ile Arg	
130 135 140	
gaa agt gaa agc caa aaa gga gaa ttc tct ctt tca gtt tta gat gga	842
Glu Ser Glu Ser Gln Lys Gly Glu Phe Ser Leu Ser Val Leu Asp Gly	
145 150 155	
gca gtt gta aaa cac tac aga att aaa aga ctg gat gaa ggg gga ttt	890
Ala Val Val Lys His Tyr Arg Ile Lys Arg Leu Asp Glu Gly Gly Phe	
160 165 170 175	
ttt ctc acg cga aga aga atc ttt tca aca ctg aac gaa ttt gtg agc	938
Phe Leu Thr Arg Arg Arg Ile Phe Ser Thr Leu Asn Glu Phe Val Ser	
180 185 190	
cac tac acc aag aca agt gac ggc ctg tgt gtc aag ctg ggg aaa cca	986
His Tyr Thr Lys Thr Ser Asp Gly Leu Cys Val Lys Leu Gly Lys Pro	
195 200 205	
tgc tta aag atc cag gtc cca gct cca ttt gat ttg tgc tat aaa acc	1034
Cys Leu Lys Ile Gln Val Pro Ala Pro Phe Asp Leu Ser Tyr Lys Thr	
210 215 220	
gtg gac caa tgg gag ata gac cgc aac tcc ata cag ctt ctg aag cga	1082
Val Asp Gln Trp Glu Ile Asp Arg Asn Ser Ile Gln Leu Leu Lys Arg	
225 230 235	
ttg gga tct ggt cag ttt ggc gaa gta tgg gaa ggt ctg tgg aac aat	1130
Leu Gly Ser Gly Gln Phe Gly Glu Val Trp Glu Gly Leu Trp Asn Asn	
240 245 250 255	
acc act cca gta gca gtg aaa aca tta aaa cca ggt tca atg gat cca	1178
Thr Thr Pro Val Ala Val Lys Thr Leu Lys Pro Gly Ser Met Asp Pro	
260 265 270	
aat gac ttc ctg agg gag gca cag ata atg aag aac cta aga cat cca	1226
Asn Asp Phe Leu Arg Glu Ala Gln Ile Met Lys Asn Leu Arg His Pro	
275 280 285	
aag ctt atc cag ctt tat gct gtt tgc act tta gaa gat cca att tat	1274
Lys Leu Ile Gln Leu Tyr Ala Val Cys Thr Leu Glu Asp Pro Ile Tyr	
290 295 300	
att att aca gag ttg atg aga cat gga agt ctg caa gaa tat ctc caa	1322
Ile Ile Thr Glu Leu Met Arg His Gly Ser Leu Gln Glu Tyr Leu Gln	
305 310 315	
aat gac act gga tca aaa atc cat ctg act caa cag gta gac atg gcg	1370
Asn Asp Thr Gly Ser Lys Ile His Leu Thr Gln Gln Val Asp Met Ala	
320 325 330 335	
gca cag gtt gcc tct gga atg gcc tat ctg gag tct cgg aac tac att	1418
Ala Gln Val Ala Ser Gly Met Ala Tyr Leu Glu Ser Arg Asn Tyr Ile	
340 345 350	

14

cac aga gat ctg gct gcc aga aat gtc ctc gtt ggt gaa cat aat atc 1466
 His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Gly Glu His Asn Ile
 355 360 365

tac aaa gta gca gat ttt gga ctt gcc aga gtt ttt aag gta gat aat 1514
 Tyr Lys Val Ala Asp Phe Gly Leu Ala Arg Val Phe Lys Val Asp Asn
 370 375 380

gaa gac atc tat gaa tct aga cac gaa ata aag ctg ccg gtg aag tgg 1562
 Glu Asp Ile Tyr Glu Ser Arg His Glu Ile Lys Leu Pro Val Lys Trp
 385 390 395

act gcg ccc gaa gcc att cgt agt aat aaa ttc agc att aag tcc gat 1610
 Thr Ala Pro Glu Ala Ile Arg Ser Asn Lys Phe Ser Ile Lys Ser Asp
 400 405 410 415

gta tgg tca ttt gga atc ctt ctt tat gaa atc att act tat ggc aaa 1658
 Val Trp Ser Phe Gly Ile Leu Leu Tyr Glu Ile Ile Thr Tyr Gly Lys
 420 425 430

atg cct tac agt ggt atg aca ggt gcc cag gta atc cag atg ttg gct 1706
 Met Pro Tyr Ser Gly Met Thr Gly Ala Gln Val Ile Gln Met Leu Ala
 435 440 445

caa aac tat aga ctt ccg caa cca tcc aac tgt cca cag caa ttt tac 1754
 Gln Asn Tyr Arg Leu Pro Gln Pro Ser Asn Cys Pro Gln Gln Phe Tyr
 450 455 460

aac atc atg ttg gag tgc tgg aat gca gag cct aag gaa cga cct aca 1802
 Asn Ile Met Leu Glu Cys Trp Asn Ala Glu Pro Lys Glu Arg Pro Thr
 465 470 475

ttt gag aca ctg cgt tgg aaa ctt gaa gac tat ttt gaa aca gac tct 1850
 Phe Glu Thr Leu Arg Trp Lys Leu Glu Asp Tyr Phe Glu Thr Asp Ser
 480 485 490 495

tca tat tca gat gca aat aac ttc ata aga tgaacactgg agaagaatat 1900
 Ser Tyr Ser Asp Ala Asn Asn Phe Ile Arg
 500 505

caaataataa agtagcaaaa caaattcaaa taatccattc caaaatacaa tgttatcaac 1960
 caactgcaca atcagtttat cctgacatat tcaagtgata ggataaagtt ggccatgtat 2020
 tatgaaaaag attattttgtg cattttattg actgggcaac actgcaggac agtcaaggtc 2080
 atatataatt gctcactgcc tggaaaatta agcacactaa accaagttat ttttcttttt 2140
 aagagatact tacattttcca tttattgttt gaaatgtcgc gatcaagaga atcaacagat 2200
 gatagtccaa tttttactca gtgatgactg tgtagcattt tctgttttac tgattagagt 2260
 ggttattcat tattcctcag attgctgaat cccatcaggc tgttattatg aaggaatttg 2320
 attgctttgc tgcacagcag gacctgtgct ttgagatttt ttttctctt ttaaaatata 2380
 ctgtaactac aatgatggta aagccatggt aaatgacttg attgtacttg gagtaattgc 2440

15

acattttttt ctatgcataa aaaaatgatg cagctgttga gaaaacgaag tctttttcat 2500
 tttgcagaag gaaatgatgg aatttttctg tacttcagta tgtgtcaact gagagtcata 2560
 tacattagtt ttaatctctt aatattgaga atcaggttgc aaaacggatg agttattatc 2620
 tatggaaatg tgagaaatgt ctaatagccc ataaagtctg agaaataggt atcaaaatag 2680
 tttaggaaaa tgagaggaga acagtaggat tgctgtggcc tagacttctg agtaattaat 2740
 aaagaaaaag aagtaccaaa aaaaaaaaaa 2770

<210> 6

<211> 505

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Megakaryocyte
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<400> 6

Met	Ser	Asn	Ile	Cys	Gln	Arg	Leu	Trp	Glu	Tyr	Leu	Glu	Pro	Tyr	Leu	1	5	10	15
Pro	Cys	Leu	Ser	Thr	Glu	Ala	Asp	Lys	Ser	Thr	Val	Ile	Glu	Asn	Pro	20	25	30	
Gly	Ala	Leu	Cys	Ser	Pro	Gln	Ser	Gln	Arg	His	Gly	His	Tyr	Phe	Val	35	40	45	
Ala	Leu	Phe	Asp	Tyr	Gln	Ala	Arg	Thr	Ala	Glu	Asp	Leu	Ser	Phe	Arg	50	55	60	
Ala	Gly	Asp	Lys	Leu	Gln	Val	Leu	Asp	Thr	Leu	His	Glu	Gly	Trp	Trp	65	70	75	80
Phe	Ala	Arg	His	Leu	Glu	Lys	Arg	Arg	Asp	Gly	Ser	Ser	Gln	Gln	Leu	85	90	95	
Gln	Gly	Tyr	Ile	Pro	Ser	Asn	Tyr	Val	Ala	Glu	Asp	Arg	Ser	Leu	Gln	100	105	110	
Ala	Glu	Pro	Trp	Phe	Phe	Gly	Ala	Ile	Gly	Arg	Ser	Asp	Ala	Glu	Lys	115	120	125	
Gln	Leu	Leu	Tyr	Ser	Glu	Asn	Lys	Thr	Gly	Ser	Phe	Leu	Ile	Arg	Glu	130	135	140	
Ser	Glu	Ser	Gln	Lys	Gly	Glu	Phe	Ser	Leu	Ser	Val	Leu	Asp	Gly	Ala	145	150	155	160
Val	Val	Lys	His	Tyr	Arg	Ile	Lys	Arg	Leu	Asp	Glu	Gly	Gly	Phe	Phe	165	170	175	
Leu	Thr	Arg	Arg	Arg	Ile	Phe	Ser	Thr	Leu	Asn	Glu	Phe	Val	Ser	His	180	185	190	

Tyr Thr Lys Thr Ser Asp Gly Leu Cys Val Lys Leu Gly Lys Pro Cys
 195 200 205
 Leu Lys Ile Gln Val Pro Ala Pro Phe Asp Leu Ser Tyr Lys Thr Val
 210 215 220
 Asp Gln Trp Glu Ile Asp Arg Asn Ser Ile Gln Leu Leu Lys Arg Leu
 225 230 235 240
 Gly Ser Gly Gln Phe Gly Glu Val Trp Glu Gly Leu Trp Asn Asn Thr
 245 250 255
 Thr Pro Val Ala Val Lys Thr Leu Lys Pro Gly Ser Met Asp Pro Asn
 260 265 270
 Asp Phe Leu Arg Glu Ala Gln Ile Met Lys Asn Leu Arg His Pro Lys
 275 280 285
 Leu Ile Gln Leu Tyr Ala Val Cys Thr Leu Glu Asp Pro Ile Tyr Ile
 290 295 300
 Ile Thr Glu Leu Met Arg His Gly Ser Leu Gln Glu Tyr Leu Gln Asn
 305 310 315 320
 Asp Thr Gly Ser Lys Ile His Leu Thr Gln Gln Val Asp Met Ala Ala
 325 330 335
 Gln Val Ala Ser Gly Met Ala Tyr Leu Glu Ser Arg Asn Tyr Ile His
 340 345 350
 Arg Asp Leu Ala Ala Arg Asn Val Leu Val Gly Glu His Asn Ile Tyr
 355 360 365
 Lys Val Ala Asp Phe Gly Leu Ala Arg Val Phe Lys Val Asp Asn Glu
 370 375 380
 Asp Ile Tyr Glu Ser Arg His Glu Ile Lys Leu Pro Val Lys Trp Thr
 385 390 395 400
 Ala Pro Glu Ala Ile Arg Ser Asn Lys Phe Ser Ile Lys Ser Asp Val
 405 410 415
 Trp Ser Phe Gly Ile Leu Leu Tyr Glu Ile Ile Thr Tyr Gly Lys Met
 420 425 430
 Pro Tyr Ser Gly Met Thr Gly Ala Gln Val Ile Gln Met Leu Ala Gln
 435 440 445
 Asn Tyr Arg Leu Pro Gln Pro Ser Asn Cys Pro Gln Gln Phe Tyr Asn
 450 455 460
 Ile Met Leu Glu Cys Trp Asn Ala Glu Pro Lys Glu Arg Pro Thr Phe
 465 470 475 480
 Glu Thr Leu Arg Trp Lys Leu Glu Asp Tyr Phe Glu Thr Asp Ser Ser
 485 490 495

17

Tyr Ser Asp Ala Asn Asn Phe Ile Arg
500 505

<210> 7
<211> 450
<212> PRT
<213> Homo sapiens

<400> 7

Met Ser Ala Ile Gln Ala Ala Trp Pro Ser Gly Thr Glu Cys Ile Ala
1 5 10 15

Lys Tyr Asn Phe His Gly Thr Ala Glu Gln Asp Leu Pro Phe Cys Lys
20 25 30

Gly Asp Val Leu Thr Ile Val Ala Val Thr Lys Asp Pro Asn Trp Tyr
35 40 45

Lys Ala Lys Asn Lys Val Gly Arg Glu Gly Ile Ile Pro Ala Asn Tyr
50 55 60

Val Gln Lys Arg Glu Gly Val Lys Ala Gly Thr Lys Leu Ser Leu Met
65 70 75 80

Pro Trp Phe His Gly Lys Ile Thr Arg Glu Gln Ala Glu Arg Leu Leu
85 90 95

Tyr Pro Pro Glu Thr Gly Leu Phe Leu Val Arg Glu Ser Thr Asn Tyr
100 105 110

Pro Gly Asp Tyr Thr Leu Cys Val Ser Cys Asp Gly Lys Val Glu His
115 120 125

Tyr Arg Ile Met Tyr His Ala Ser Lys Leu Ser Ile Asp Glu Glu Val
130 135 140

Tyr Phe Glu Asn Leu Met Gln Leu Val Glu His Tyr Thr Ser Asp Ala
145 150 155 160

Asp Gly Leu Cys Thr Arg Leu Ile Lys Pro Lys Val Met Glu Gly Thr
165 170 175

Val Ala Ala Gln Asp Glu Phe Tyr Arg Ser Gly Trp Ala Leu Asn Met
180 185 190

Lys Glu Leu Lys Leu Leu Gln Thr Ile Gly Lys Gly Glu Phe Gly Asp
195 200 205

Val Met Leu Gly Asp Tyr Arg Gly Asn Lys Val Ala Val Lys Cys Ile
210 215 220

Lys Asn Asp Ala Thr Ala Gln Ala Phe Leu Ala Glu Ala Ser Val Met
225 230 235 240

Thr Gln Leu Arg His Ser Asn Leu Val Gln Leu Leu Gly Val Ile Val
245 250 255

18

Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr Met Ala Lys Gly
 260 265 270
 Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser Val Leu Gly Gly
 275 280 285
 Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu Ala Met Glu Tyr
 290 295 300
 Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala Ala Arg Asn Val
 305 310 315 320
 Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp Phe Gly Leu Thr
 325 330 335
 Lys Glu Ala Ser Ser Thr Gln Asp Thr Gly Lys Leu Pro Val Lys Trp
 340 345 350
 Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser Thr Lys Ser Asp
 355 360 365
 Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Tyr Ser Phe Gly Arg
 370 375 380
 Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val Pro Arg Val Glu
 385 390 395 400
 Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro Pro Ala Val Tyr
 405 410 415
 Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala Met Arg Pro Ser
 420 425 430
 Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys Thr His Glu Leu
 435 440 445
 His Leu
 450

<210> 8

<211> 659

<212> PRT

<213> Homo sapiens

<400> 8

Met Ala Ala Val Ile Leu Glu Ser Ile Phe Leu Lys Arg Ser Gln Gln
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 Lys Lys Lys Thr Ser Pro Leu Asn Phe Lys Lys Arg Leu Phe Leu Leu
 20 25 30
 Thr Val His Lys Leu Ser Tyr Tyr Glu Tyr Asp Phe Glu Arg Gly Arg
 35 40 45
 Arg Gly Ser Lys Lys Gly Ser Ile Asp Val Glu Lys Ile Thr Cys Val
 50 55 60

Glu Thr Val Val Pro Glu Lys Asn Pro Pro Pro Glu Arg Gln Ile Pro
 65 70 75 80
 Arg Arg Gly Glu Glu Ser Ser Glu Met Glu Gln Ile Ser Ile Ile Glu
 85 90 95
 Arg Phe Pro Tyr Pro Phe Gln Val Val Tyr Asp Glu Gly Pro Leu Tyr
 100 105 110
 Val Phe Ser Pro Thr Glu Glu Leu Arg Lys Arg Trp Ile His Gln Leu
 115 120 125
 Lys Asn Val Ile Arg Tyr Asn Ser Asp Leu Val Gln Lys Tyr His Pro
 130 135 140
 Cys Phe Trp Ile Asp Gly Gln Tyr Leu Cys Cys Ser Gln Thr Ala Lys
 145 150 155 160
 Asn Ala Met Gly Cys Gln Ile Leu Glu Asn Arg Asn Gly Ser Leu Lys
 165 170 175
 Pro Gly Ser Ser His Arg Lys Thr Lys Lys Pro Leu Pro Pro Thr Pro
 180 185 190
 Glu Glu Asp Gln Ile Leu Lys Lys Pro Leu Pro Pro Glu Pro Ala Ala
 195 200 205
 Ala Pro Val Ser Thr Ser Glu Leu Lys Lys Val Val Ala Leu Tyr Asp
 210 215 220
 Tyr Met Pro Met Asn Ala Asn Asp Leu Gln Leu Arg Lys Gly Asp Glu
 225 230 235 240
 Tyr Phe Ile Leu Glu Glu Ser Asn Leu Pro Trp Trp Arg Ala Arg Asp
 245 250 255
 Lys Asn Gly Gln Glu Gly Tyr Ile Pro Ser Asn Tyr Val Thr Glu Ala
 260 265 270
 Glu Asp Ser Ile Glu Met Tyr Glu Trp Tyr Ser Lys His Met Thr Arg
 275 280 285
 Ser Gln Ala Glu Gln Leu Leu Lys Gln Glu Gly Lys Glu Gly Gly Phe
 290 295 300
 Ile Val Arg Asp Ser Ser Lys Ala Gly Lys Tyr Thr Val Ser Val Phe
 305 310 315 320
 Ala Lys Ser Thr Gly Asp Pro Gln Gly Val Ile Arg His Tyr Val Val
 325 330 335
 Cys Ser Thr Pro Gln Ser Gln Tyr Tyr Leu Ala Glu Lys His Leu Phe
 340 345 350
 Ser Thr Ile Pro Glu Leu Ile Asn Tyr His Gln His Asn Ser Ala Gly
 355 360 365

Leu Ile Ser Arg Leu Lys Tyr Pro Val Ser Gln Gln Asn Lys Asn Ala
 370 375 380
 Pro Ser Thr Ala Gly Leu Gly Tyr Gly Ser Trp Glu Ile Asp Pro Lys
 385 390 395 400
 Asp Leu Thr Phe Leu Lys Glu Leu Gly Thr Gly Gln Phe Gly Val Val
 405 410 415
 Lys Tyr Gly Lys Trp Arg Gly Gln Tyr Asp Val Ala Ile Lys Met Ile
 420 425 430
 Lys Glu Gly Ser Met Ser Glu Asp Glu Phe Ile Glu Glu Ala Lys Val
 435 440 445
 Met Met Asn Leu Ser His Glu Lys Leu Val Gln Leu Tyr Gly Val Cys
 450 455 460
 Thr Lys Gln Arg Pro Ile Phe Ile Ile Thr Glu Tyr Met Ala Asn Gly
 465 470 475 480
 Cys Leu Leu Asn Tyr Leu Arg Glu Met Arg His Arg Phe Gln Thr Gln
 485 490 495
 Gln Leu Leu Glu Met Cys Lys Asp Val Cys Glu Ala Met Glu Tyr Leu
 500 505 510
 Glu Ser Lys Gln Phe Leu His Arg Asp Leu Ala Ala Arg Asn Cys Leu
 515 520 525
 Val Asn Asp Gln Gly Val Val Lys Val Ser Asp Phe Gly Leu Ser Arg
 530 535 540
 Tyr Val Leu Asp Asp Glu Tyr Thr Ser Ser Val Gly Ser Lys Phe Pro
 545 550 555 560
 Val Arg Trp Ser Pro Pro Glu Val Leu Met Tyr Ser Lys Phe Ser Ser
 565 570 575
 Lys Ser Asp Ile Trp Ala Phe Gly Val Leu Met Trp Glu Ile Tyr Ser
 580 585 590
 Leu Gly Lys Met Pro Tyr Glu Arg Phe Thr Asn Ser Glu Thr Ala Glu
 595 600 605
 His Ile Ala Gln Gly Leu Arg Leu Tyr Arg Pro His Leu Ala Ser Glu
 610 615 620
 Lys Val Tyr Thr Ile Met Tyr Ser Cys Trp His Glu Lys Ala Asp Glu
 625 630 635 640
 Arg Pro Thr Phe Lys Ile Leu Leu Ser Asn Ile Leu Asp Val Met Asp
 645 650 655
 Glu Glu Ser

21

<210> 9

<211> 620

<212> PRT

<213> Homo sapiens

<400> 9

Met Asn Asn Phe Ile Leu Leu Glu Glu Gln Leu Ile Lys Lys Ser Gln
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Gln Lys Arg Arg Thr Ser Pro Ser Asn Phe Lys Val Arg Phe Phe Val
 20 25 30

Leu Thr Lys Ala Ser Leu Ala Tyr Phe Glu Asp Arg His Gly Lys Lys
 35 40 45

Arg Thr Leu Lys Gly Ser Ile Glu Leu Ser Arg Ile Lys Cys Val Glu
 50 55 60

Ile Val Lys Ser Asp Ile Ser Ile Pro Cys His Tyr Lys Tyr Pro Phe
 65 70 75 80

Gln Val Val His Asp Asn Tyr Leu Leu Tyr Val Phe Ala Pro Asp Arg
 85 90 95

Glu Ser Arg Gln Arg Trp Val Leu Ala Leu Lys Glu Glu Thr Arg Asn
 100 105 110

Asn Asn Ser Leu Val Pro Lys Tyr His Pro Asn Phe Trp Met Asp Gly
 115 120 125

Lys Trp Arg Cys Cys Ser Gln Leu Glu Lys Leu Ala Thr Gly Cys Ala
 130 135 140

Gln Tyr Asp Pro Thr Lys Asn Ala Ser Lys Lys Pro Leu Pro Pro Thr
 145 150 155 160

Pro Glu Asp Asn Arg Arg Pro Leu Trp Glu Pro Glu Glu Thr Val Val
 165 170 175

Ile Ala Leu Tyr Asp Tyr Gln Thr Asn Asp Pro Gln Glu Leu Ala Leu
 180 185 190

Arg Arg Asn Glu Glu Tyr Cys Leu Leu Asp Ser Ser Glu Ile His Trp
 195 200 205

Trp Arg Val Gln Asp Arg Asn Gly His Glu Gly Tyr Val Pro Ser Ser
 210 215 220

Tyr Leu Val Glu Lys Ser Pro Asn Asn Leu Glu Thr Tyr Glu Trp Tyr
 225 230 235 240

Asn Lys Ser Ile Ser Arg Asp Lys Ala Glu Lys Leu Leu Leu Asp Thr
 245 250 255

Gly Lys Glu Gly Ala Phe Met Val Arg Asp Ser Arg Thr Ala Gly Thr
 260 265 270

Tyr Thr Val Ser Val Phe Thr Lys Ala Val Val Ser Glu Asn Asn Pro
 275 280 285
 Cys Ile Lys His Tyr His Ile Lys Glu Thr Asn Asp Asn Pro Lys Arg
 290 295 300
 Tyr Tyr Val Ala Glu Lys Tyr Val Phe Asp Ser Ile Pro Leu Leu Ile
 305 310 315 320
 Asn Tyr His Gln His Asn Gly Gly Gly Leu Val Thr Arg Leu Arg Tyr
 325 330 335
 Pro Val Cys Phe Gly Arg Gln Lys Ala Pro Val Thr Ala Gly Leu Arg
 340 345 350
 Tyr Gly Lys Trp Val Ile Asp Pro Ser Glu Leu Thr Phe Val Gln Glu
 355 360 365
 Ile Gly Ser Gly Gln Phe Gly Leu Val His Leu Gly Tyr Trp Leu Asn
 370 375 380
 Lys Asp Lys Val Ala Ile Lys Thr Ile Arg Glu Gly Ala Met Ser Glu
 385 390 395 400
 Glu Asp Phe Ile Glu Glu Ala Glu Val Met Met Lys Leu Ser His Pro
 405 410 415
 Lys Leu Val Gln Leu Tyr Gly Val Cys Leu Glu Gln Ala Pro Ile Cys
 420 425 430
 Leu Val Phe Glu Phe Met Glu His Gly Cys Leu Ser Asp Tyr Leu Arg
 435 440 445
 Thr Gln Arg Gly Leu Phe Ala Ala Glu Thr Leu Leu Gly Met Cys Leu
 450 455 460
 Asp Val Cys Glu Gly Met Ala Tyr Leu Glu Glu Ala Cys Val Ile His
 465 470 475 480
 Arg Asp Leu Ala Ala Arg Asn Cys Leu Val Gly Glu Asn Gln Val Ile
 485 490 495
 Lys Val Ser Asp Phe Gly Met Thr Arg Phe Val Leu Asp Asp Gln Tyr
 500 505 510
 Thr Ser Ser Thr Gly Thr Lys Phe Pro Val Lys Trp Ala Ser Pro Glu
 515 520 525
 Val Phe Ser Phe Ser Arg Tyr Ser Ser Lys Ser Asp Val Trp Ser Phe
 530 535 540
 Gly Val Leu Met Trp Glu Val Phe Ser Glu Gly Lys Ile Pro Tyr Glu
 545 550 555 560
 Asn Arg Ser Asn Ser Glu Val Val Glu Asp Ile Ser Thr Gly Phe Arg
 565 570 575

23

Leu Tyr Lys Pro Arg Leu Ala Ser Thr His Val Tyr Gln Ile Met Asn
 580 585 590

His Cys Trp Lys Glu Arg Pro Glu Asp Arg Pro Ala Phe Ser Arg Leu
 595 600 605

Leu Arg Gln Leu Ala Glu Ile Ala Glu Ser Gly Leu
 610 615 620

<210> 10
 <211> 527
 <212> PRT
 <213> Mus sp.

<400> 10

Met Met Val Ser Phe Pro Val Lys Ile Asn Phe His Ser Ser Pro Gln
 1 5 10 15

Ser Arg Asp Arg Trp Val Lys Lys Leu Lys Glu Glu Ile Lys Asn Asn
 20 25 30

Asn Asn Ile Met Ile Lys Tyr His Pro Lys Phe Trp Ala Asp Gly Ser
 35 40 45

Tyr Gln Cys Cys Arg Gln Thr Glu Lys Leu Ala Pro Gly Cys Glu Lys
 50 55 60

Tyr Asn Leu Phe Glu Ser Ser Ile Arg Lys Thr Leu Pro Pro Ala Pro
 65 70 75 80

Glu Ile Lys Lys Arg Arg Pro Pro Pro Pro Ile Pro Pro Glu Glu Glu
 85 90 95

Asn Thr Glu Glu Ile Val Val Ala Met Tyr Asp Phe Gln Ala Thr Glu
 100 105 110

Ala His Asp Leu Arg Leu Glu Arg Gly Gln Glu Tyr Ile Ile Leu Glu
 115 120 125

Lys Asn Asp Leu His Trp Trp Arg Ala Arg Asp Lys Tyr Gly Trp Tyr
 130 135 140

Cys Arg Asn Thr Asn Arg Ser Lys Ala Glu Gln Leu Leu Arg Thr Glu
 145 150 155 160

Asp Lys Glu Gly Gly Phe Met Val Arg Asp Ser Ser Gln Pro Gly Leu
 165 170 175

Tyr Thr Val Ser Leu Tyr Thr Lys Phe Gly Gly Glu Gly Ser Ser Gly
 180 185 190

Phe Arg His Tyr His Ile Lys Glu Thr Ala Thr Ser Pro Lys Lys Tyr
 195 200 205

Tyr Leu Ala Glu Lys His Ala Phe Gly Ser Ile Pro Glu Ile Ile Glu
 210 215 220

Tyr His Lys His Asn Ala Ala Gly Leu Val Thr Arg Leu Arg Tyr Pro
 225 230 235 240
 Val Ser Thr Lys Gly Lys Asn Ala Pro Thr Thr Ala Gly Phe Ser Tyr
 245 250 255
 Asp Lys Trp Glu Ile Asn Pro Ser Glu Leu Thr Phe Met Arg Glu Leu
 260 265 270
 Gly Ser Gly Leu Phe Gly Val Val Arg Leu Gly Lys Trp Arg Ala Gln
 275 280 285
 Tyr Lys Val Ala Ile Lys Ala Ile Arg Glu Gly Ala Met Cys Glu Glu
 290 295 300
 Asp Phe Ile Glu Glu Ala Lys Val Met Met Lys Leu Thr His Pro Lys
 305 310 315 320
 Leu Val Gln Leu Tyr Gly Val Cys Thr Gln Gln Lys Pro Ile Tyr Ile
 325 330 335
 Val Thr Glu Phe Met Glu Arg Gly Cys Leu Leu Asn Phe Leu Arg Gln
 340 345 350
 Arg Gln Gly His Phe Ser Arg Asp Met Leu Leu Ser Met Cys Gln Asp
 355 360 365
 Val Cys Glu Gly Met Glu Tyr Leu Glu Arg Asn Ser Phe Ile His Arg
 370 375 380
 Asp Leu Ala Ala Arg Asn Cys Leu Val Asn Glu Ala Gly Val Val Lys
 385 390 395 400
 Val Ser Asp Phe Gly Met Ala Arg Tyr Val Leu Asp Asp Gln Tyr Thr
 405 410 415
 Ser Ser Ser Gly Ala Lys Phe Pro Val Lys Trp Cys Pro Pro Glu Val
 420 425 430
 Phe Asn Tyr Ser Arg Phe Ser Ser Lys Ser Asp Val Trp Ser Phe Gly
 435 440 445
 Val Leu Met Trp Glu Ile Phe Thr Glu Gly Arg Met Pro Phe Glu Lys
 450 455 460
 Asn Thr Asn Tyr Glu Val Val Thr Met Val Thr Arg Gly His Arg Leu
 465 470 475 480
 His Arg Pro Lys Leu Ala Thr Lys Tyr Leu Tyr Glu Val Met Leu Arg
 485 490 495
 Cys Trp Gln Glu Arg Pro Glu Gly Arg Pro Ser Phe Glu Asp Leu Leu
 500 505 510
 Arg Thr Ile Asp Glu Leu Val Glu Cys Glu Glu Thr Phe Gly Arg
 515 520 525

25

<210> 11

<211> 537

<212> PRT

<213> Homo sapiens

<400> 11

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Met Gly Cys Val Gln Cys Lys Asp Lys Glu Ala Thr Lys Leu Thr Glu
 1          5          10          15

Glu Arg Asp Gly Ser Leu Asn Gln Ser Ser Gly Tyr Arg Tyr Gly Thr
          20          25          30

Asp Pro Thr Pro Gln His Tyr Pro Ser Phe Gly Val Thr Ser Ile Pro
          35          40          45

Asn Tyr Asn Asn Phe His Ala Ala Gly Gly Gln Gly Leu Thr Val Phe
          50          55          60

Gly Gly Val Asn Ser Ser Ser His Thr Gly Thr Leu Arg Thr Arg Gly
          65          70          75          80

Gly Thr Gly Val Thr Leu Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg
          85          90          95

Thr Glu Asp Asp Leu Ser Phe His Lys Gly Glu Lys Phe Gln Ile Leu
          100          105          110

Asn Ser Ser Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Thr Thr Gly
          115          120          125

Glu Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile
          130          135          140

Gln Ala Glu Glu Trp Tyr Phe Gly Lys Leu Gly Arg Lys Asp Ala Glu
          145          150          155          160

Arg Gln Leu Leu Ser Phe Gly Asn Pro Arg Gly Thr Phe Leu Ile Arg
          165          170          175

Glu Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp
          180          185          190

Asp Asp Met Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu
          195          200          205

Asp Asn Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Glu Thr Leu
          210          215          220

Gln Gln Leu Val Gln His Tyr Ser Glu Arg Ala Ala Gly Leu Cys Cys
          225          230          235          240

Arg Leu Val Val Pro Cys His Lys Gly Met Pro Arg Leu Thr Asp Leu
          245          250          255

Ser Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln
          260          265          270

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26

Leu Ile Lys Arg Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly
 275 280 285
 Thr Trp Asn Gly Asn Thr Lys Val Ala Ile Lys Thr Leu Lys Pro Gly
 290 295 300
 Thr Met Ser Pro Glu Ser Phe Leu Glu Glu Ala Gln Ile Met Lys Lys
 305 310 315 320
 Leu Lys His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu
 325 330 335
 Pro Ile Tyr Ile Val Thr Glu Tyr Met Asn Lys Gly Ser Leu Leu Asp
 340 345 350
 Phe Leu Lys Asp Gly Glu Gly Arg Ala Leu Lys Leu Pro Asn Leu Val
 355 360 365
 Asp Met Ala Ala Gln Val Ala Ala Gly Met Ala Tyr Ile Glu Arg Met
 370 375 380
 Asn Tyr Ile His Arg Asp Leu Arg Ser Ala Asn Ile Leu Val Gly Asn
 385 390 395 400
 Gly Leu Ile Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu
 405 410 415
 Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp
 420 425 430
 Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp
 435 440 445
 Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg
 450 455 460
 Val Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu
 465 470 475 480
 Arg Gly Tyr Arg Met Pro Cys Pro Gln Asp Cys Pro Ile Ser Leu His
 485 490 495
 Glu Leu Met Ile His Cys Trp Lys Lys Asp Pro Glu Glu Arg Pro Thr
 500 505 510
 Phe Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu
 515 520 525
 Pro Gln Tyr Gln Pro Gly Glu Asn Leu
 530 535

<210> 12

<211> 536

<212> PRT

<213> Gallus gallus

27

<400> 12

Met Gly Cys Val His Cys Lys Glu Lys Ile Ser Gly Lys Gly Gln Gly
 1 5 10 15
 Gly Ser Gly Thr Gly Thr Pro Ala His Pro Pro Ser Gln Tyr Asp Pro
 20 25 30
 Asp Pro Thr Gln Leu Ser Gly Ala Phe Thr His Ile Pro Asp Phe Asn
 35 40 45
 Asn Phe His Ala Ala Ala Val Ser Pro Pro Val Pro Phe Ser Gly Pro
 50 55 60
 Gly Phe Tyr Pro Cys Asn Thr Leu Gln Ala His Ser Ser Ile Thr Gly
 65 70 75 80
 Gly Gly Val Thr Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr
 85 90 95
 Glu Asp Asp Leu Ser Phe Gln Lys Gly Glu Lys Phe His Ile Ile Asn
 100 105 110
 Asn Thr Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Ala
 115 120 125
 Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln
 130 135 140
 Ala Glu Glu Trp Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg
 145 150 155 160
 Gln Leu Leu Cys His Gly Asn Cys Arg Gly Thr Phe Leu Ile Arg Glu
 165 170 175
 Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp
 180 185 190
 Glu Ala Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp
 195 200 205
 Ser Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Asp Thr Ile Gln
 210 215 220
 Gln Leu Val Gln His Tyr Ile Glu Arg Ala Ala Gly Leu Cys Cys Arg
 225 230 235 240
 Leu Ala Val Pro Cys Pro Lys Gly Thr Pro Lys Leu Ala Asp Leu Ser
 245 250 255
 Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln Leu
 260 265 270
 Leu Gln Lys Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly Thr
 275 280 285
 Trp Asn Gly Thr Thr Lys Val Ala Val Lys Thr Leu Lys Pro Gly Thr
 290 295 300

28

Met Ser Pro Glu Ala Phe Leu Glu Glu Ala Gln Ile Met Lys Arg Leu
 305 310 315 320
 Arg His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
 325 330 335
 Ile Tyr Ile Val Thr Glu Phe Met Ser Gln Gly Ser Leu Leu Asp Phe
 340 345 350
 Leu Lys Asp Gly Asp Gly Arg Tyr Leu Lys Leu Pro Gln Leu Val Asp
 355 360 365
 Met Ala Ala Gln Ile Ala Ala Gly Met Ala Tyr Ile Glu Arg Met Asn
 370 375 380
 Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Asp Asn
 385 390 395 400
 Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
 405 410 415
 Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
 420 425 430
 Ala Pro Glu Ala Ala Leu Phe Gly Lys Phe Thr Ile Lys Ser Asp Val
 435 440 445
 Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg Val
 450 455 460
 Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu Arg
 465 470 475 480
 Gly Tyr Arg Met Gln Cys Pro Gly Gly Cys Pro Pro Ser Leu His Asp
 485 490 495
 Val Met Val Gln Cys Trp Lys Arg Glu Pro Glu Glu Arg Pro Thr Phe
 500 505 510
 Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro
 515 520 525
 Gln Tyr Gln Pro Gly Asp Asn Gln
 530 535

<210> 13
 <211> 536
 <212> PRT
 <213> Homo sapiens

<400> 13
 Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg
 1 5 10 15
 Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe
 20 25 30

Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg
 35 40 45
 Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe
 50 55 60
 Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly
 65 70 75 80
 Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu
 85 90 95
 Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln
 100 105 110
 Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser
 115 120 125
 Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp
 130 135 140
 Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu
 145 150 155 160
 Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu
 165 170 175
 Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser
 180 185 190
 Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg
 195 200 205
 Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn
 210 215 220
 Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu
 225 230 235 240
 Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln
 245 250 255
 Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu
 260 265 270
 Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr
 275 280 285
 Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr
 290 295 300
 Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu
 305 310 315 320
 Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
 325 330 335

30

Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe
 340 345 350
 Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp
 355 360 365
 Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn
 370 375 380
 Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn
 385 390 395 400
 Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
 405 410 415
 Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
 420 425 430
 Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val
 435 440 445
 Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val
 450 455 460
 Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg
 465 470 475 480
 Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp
 485 490 495
 Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe
 500 505 510
 Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro
 515 520 525
 Gln Tyr Gln Pro Gly Glu Asn Leu
 530 535

<210> 14

<211> 543

<212> PRT

<213> Homo sapiens

<400> 14

Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr
 1 5 10 15
 Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr
 20 25 30
 Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ser Ala Lys
 35 40 45
 Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly
 50 55 60

Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val
 65 70 75 80
 Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe
 85 90 95
 Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe
 100 105 110
 Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp
 115 120 125
 Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser
 130 135 140
 Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe
 145 150 155 160
 Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu Asn Pro Gly
 165 170 175
 Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly
 180 185 190
 Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg Gly Asp Asn
 195 200 205
 Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile
 210 215 220
 Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val Lys His Tyr
 225 230 235 240
 Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr Val Cys Pro
 245 250 255
 Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile
 260 265 270
 Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe
 275 280 285
 Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile
 290 295 300
 Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu
 305 310 315 320
 Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr
 325 330 335
 Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe Met Ser
 340 345 350
 Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu
 355 360 365

32

Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met
 370 375 380
 Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala
 385 390 395 400
 Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly
 405 410 415
 Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala
 420 425 430
 Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg
 435 440 445
 Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu
 450 455 460
 Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu
 465 470 475 480
 Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly
 485 490 495
 Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp
 500 505 510
 Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp
 515 520 525
 Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu
 530 535 540

<210> 15
 <211> 529
 <212> PRT
 <213> Homo sapiens

<400> 15
 Met Gly Cys Val Phe Cys Lys Lys Leu Glu Pro Val Ala Thr Ala Lys
 1 5 10 15
 Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp
 20 25 30
 His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala
 35 40 45
 His Ile Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly
 50 55 60
 Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr
 65 70 75 80
 Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu
 85 90 95

Thr Phe Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly
 100 105 110
 Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Lys Thr Gly Cys Ile
 115 120 125
 Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln Ala Glu Glu Trp
 130 135 140
 Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg Gln Leu Leu Ser
 145 150 155 160
 Pro Gly Asn Pro Gln Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr Thr
 165 170 175
 Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Gln Thr Arg Gly
 180 185 190
 Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp Met Gly Gly Tyr
 195 200 205
 Tyr Ile Thr Thr Arg Val Gln Phe Asn Ser Val Gln Glu Leu Val Gln
 210 215 220
 His Tyr Met Glu Val Asn Asp Gly Leu Cys Asn Leu Leu Ile Ala Pro
 225 230 235 240
 Cys Thr Ile Met Lys Pro Gln Thr Leu Gly Leu Ala Lys Asp Ala Trp
 245 250 255
 Glu Ile Ser Arg Ser Ser Ile Thr Leu Glu Arg Arg Leu Gly Thr Gly
 260 265 270
 Cys Phe Gly Asp Val Trp Leu Gly Thr Trp Asn Gly Ser Thr Lys Val
 275 280 285
 Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Pro Lys Ala Phe Leu
 290 295 300
 Glu Glu Ala Gln Val Met Lys Leu Leu Arg His Asp Lys Leu Val Gln
 305 310 315 320
 Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe
 325 330 335
 Met Cys His Gly Ser Leu Leu Asp Phe Leu Lys Asn Pro Glu Gly Gln
 340 345 350
 Asp Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala Gln Val Ala Glu
 355 360 365
 Gly Met Ala Tyr Met Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg
 370 375 380
 Ala Ala Asn Ile Leu Val Gly Glu Arg Leu Ala Cys Lys Ile Ala Asp
 385 390 395 400

Trp Phe Phe Lys Asp Ile Thr Arg Lys Asp Ala Glu Arg Gln Leu Leu
 130 135 140
 Ala Pro Gly Asn Ser Ala Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr
 145 150 155 160
 Leu Lys Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Pro Val His
 165 170 175
 Gly Asp Val Ile Lys His Tyr Lys Ile Arg Ser Leu Asp Asn Gly Gly
 180 185 190
 Tyr Tyr Ile Ser Pro Arg Ile Thr Phe Pro Cys Ile Ser Asp Met Ile
 195 200 205
 Lys His Tyr Gln Lys Gln Ala Asp Gly Leu Cys Arg Arg Leu Glu Lys
 210 215 220
 Ala Cys Ile Ser Pro Lys Pro Gln Lys Pro Trp Asp Lys Asp Ala Trp
 225 230 235 240
 Glu Ile Pro Arg Glu Ser Ile Lys Leu Val Lys Arg Leu Gly Ala Gly
 245 250 255
 Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Asn Asn Ser Thr Lys Val
 260 265 270
 Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Val Gln Ala Phe Leu
 275 280 285
 Glu Glu Ala Asn Leu Met Lys Thr Leu Gln His Asp Lys Leu Val Arg
 290 295 300
 Leu Tyr Ala Val Val Thr Arg Glu Glu Pro Ile Tyr Ile Ile Thr Glu
 305 310 315 320
 Tyr Met Ala Lys Gly Ser Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly
 325 330 335
 Gly Lys Val Leu Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala
 340 345 350
 Glu Gly Met Ala Tyr Ile Glu Arg Lys Asn Tyr Ile His Arg Asp Leu
 355 360 365
 Arg Ala Ala Asn Val Leu Val Ser Glu Ser Leu Met Cys Lys Ile Ala
 370 375 380
 Asp Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg
 385 390 395 400
 Glu Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn
 405 410 415
 Phe Gly Cys Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu
 420 425 430

36

Leu Tyr Glu Ile Val Thr Tyr Gly Lys Ile Pro Tyr Pro Gly Arg Thr
 435 440 445

Asn Ala Asp Val Met Thr Ala Leu Ser Gln Gly Tyr Arg Met Pro Arg
 450 455 460

Val Glu Asn Cys Pro Asp Glu Leu Tyr Asp Ile Met Lys Met Cys Trp
 465 470 475 480

Lys Glu Lys Ala Glu Glu Arg Pro Thr Phe Asp Tyr Leu Gln Ser Val
 485 490 495

Leu Asp Asp Phe Tyr Thr Ala Thr Glu Gly Gln Tyr Gln Gln Gln Pro
 500 505 510

<210> 17

<211> 505

<212> PRT

<213> Homo sapiens

<400> 17

Met Gly Ser Met Lys Ser Lys Phe Leu Gln Val Gly Gly Asn Thr Phe
 1 5 10 15

Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro Val Tyr Val Pro
 20 25 30

Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser His Asn Ser Asn
 35 40 45

Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile Ile Val Val Ala
 50 55 60

Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu Ser Phe Gln Lys
 65 70 75 80

Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu Trp Trp Lys Ala
 85 90 95

Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro Ser Asn Tyr Val
 100 105 110

Ala Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe Phe Lys Gly Ile
 115 120 125

Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro Gly Asn Met Leu
 130 135 140

Gly Ser Phe Met Ile Arg Asp Ser Glu Thr Thr Lys Gly Ser Tyr Ser
 145 150 155 160

Leu Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp Thr Val Lys His
 165 170 175

Tyr Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr Ile Ser Pro Arg
 180 185 190

Ser Thr Phe Ser Thr Leu Gln Glu Leu Val Asp His Tyr Lys Lys Gly
 195 200 205
 Asn Asp Gly Leu Cys Gln Lys Leu Ser Val Pro Cys Met Ser Ser Lys
 210 215 220
 Pro Gln Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser
 225 230 235 240
 Leu Lys Leu Glu Lys Lys Leu Gly Ala Gly Gln Phe Gly Glu Val Trp
 245 250 255
 Met Ala Thr Tyr Asn Lys His Thr Lys Val Ala Val Lys Thr Met Lys
 260 265 270
 Pro Gly Ser Met Ser Val Glu Ala Phe Leu Ala Glu Ala Asn Val Met
 275 280 285
 Lys Thr Leu Gln His Asp Lys Leu Val Lys Leu His Ala Val Val Thr
 290 295 300
 Lys Glu Pro Ile Tyr Ile Ile Thr Glu Phe Met Ala Lys Gly Ser Leu
 305 310 315 320
 Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln Pro Leu Pro Lys
 325 330 335
 Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met Ala Phe Ile Glu
 340 345 350
 Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val
 355 360 365
 Ser Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Val
 370 375 380
 Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala Lys Phe Pro Ile
 385 390 395 400
 Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser Phe Thr Ile Lys
 405 410 415
 Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu Ile Val Thr Tyr
 420 425 430
 Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Ala
 435 440 445
 Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn Cys Pro Glu Glu
 450 455 460
 Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg Pro Glu Glu Arg
 465 470 475 480
 Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp Phe Tyr Thr Ala
 485 490 495

38

Thr Glu Ser Gln Tyr Gln Gln Gln Pro
500 505

<210> 18
<211> 509
<212> PRT
<213> Homo sapiens

<400> 18

Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn
1 5 10 15

Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly
20 25 30

Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu
35 40 45

Val Thr Tyr Glu Gly Ser Asn Pro Pro Ala Ser Pro Leu Gln Asp Asn
50 55 60

Leu Val Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu
65 70 75 80

Gly Phe Glu Lys Gly Glu Gln Leu Arg Ile Leu Glu Gln Ser Gly Glu
85 90 95

Trp Trp Lys Ala Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro
100 105 110

Phe Asn Phe Val Ala Lys Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe
115 120 125

Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro
130 135 140

Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala
145 150 155 160

Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Gln Asn Gln Gly Glu
165 170 175

Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly Gly Phe Tyr
180 185 190

Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Glu Leu Val Arg His
195 200 205

Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser Arg Pro Cys
210 215 220

Gln Thr Gln Lys Pro Gln Lys Pro Trp Trp Glu Asp Glu Trp Glu Val
225 230 235 240

Pro Arg Glu Thr Leu Lys Leu Val Glu Arg Leu Gly Ala Gly Gln Phe
245 250 255

39

Gly Glu Val Trp Met Gly Tyr Tyr Asn Gly His Thr Lys Val Ala Val
 260 265 270
 Lys Ser Leu Lys Gln Gly Ser Met Ser Pro Asp Ala Phe Leu Ala Glu
 275 280 285
 Ala Asn Leu Met Lys Gln Leu Gln His Gln Arg Leu Val Arg Leu Tyr
 290 295 300
 Ala Val Val Thr Gln Glu Pro Ile Tyr Ile Ile Thr Glu Tyr Met Glu
 305 310 315 320
 Asn Gly Ser Leu Val Asp Phe Leu Lys Thr Pro Ser Gly Ile Lys Leu
 325 330 335
 Thr Ile Asn Lys Leu Leu Asp Met Ala Ala Gln Ile Ala Glu Gly Met
 340 345 350
 Ala Phe Ile Glu Glu Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala
 355 360 365
 Asn Ile Leu Val Ser Asp Thr Leu Ser Cys Lys Ile Ala Asp Phe Gly
 370 375 380
 Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala
 385 390 395 400
 Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Tyr Gly Thr
 405 410 415
 Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu
 420 425 430
 Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn Pro Glu
 435 440 445
 Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro Asp Asn
 450 455 460
 Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys Glu Arg
 465 470 475 480
 Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu Asp
 485 490 495
 Phe Phe Thr Ala Thr Glu Gly Gln Tyr Gln Pro Gln Pro
 500 505

<210> 19
 <211> 499
 <212> PRT
 <213> Mus sp.

<400> 19
 Met Gly Leu Leu Ser Ser Lys Arg Gln Val Ser Glu Lys Gly Lys Gly
 1 5 10 15

40

Trp Ser Pro Val Lys Ile Arg Thr Gln Asp Lys Ala Pro Pro Pro Leu
 20 25 30

Pro Pro Leu Val Val Phe Asn His Leu Ala Pro Pro Ser Pro Asn Gln
 35 40 45

Asp Pro Asp Glu Glu Glu Arg Phe Val Val Ala Leu Phe Asp Tyr Ala
 50 55 60

Ala Val Asn Asp Arg Asp Leu Gln Val Leu Lys Gly Glu Lys Leu Gln
 65 70 75 80

Val Leu Arg Ser Thr Gly Asp Trp Trp Leu Ala Arg Ser Leu Val Thr
 85 90 95

Gly Arg Glu Gly Tyr Val Pro Ser Asn Phe Val Ala Pro Val Glu Thr
 100 105 110

Leu Glu Val Glu Lys Trp Phe Phe Arg Thr Ile Ser Arg Lys Asp Ala
 115 120 125

Glu Arg Gln Leu Leu Ala Pro Met Asn Lys Ala Gly Ser Phe Leu Ile
 130 135 140

Arg Glu Ser Glu Ser Asn Lys Gly Ala Phe Ser Leu Ser Val Lys Asp
 145 150 155 160

Ile Thr Thr Gln Gly Glu Val Val Lys His Tyr Lys Ile Arg Ser Leu
 165 170 175

Asp Asn Gly Gly Tyr Tyr Ile Ser Pro Arg Ile Thr Phe Pro Thr Leu
 180 185 190

Gln Ala Leu Val Gln His Tyr Ser Lys Lys Gly Asp Gly Leu Cys Gln
 195 200 205

Lys Leu Thr Leu Pro Cys Val Asn Leu Ala Pro Lys Asn Leu Trp Ala
 210 215 220

Gln Asp Glu Trp Glu Ile Pro Arg Gln Ser Leu Lys Leu Val Arg Lys
 225 230 235 240

Leu Gly Ser Gly Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Lys Asn
 245 250 255

Asn Met Lys Val Ala Ile Lys Thr Leu Lys Glu Gly Thr Met Ser Pro
 260 265 270

Glu Ala Phe Leu Gly Glu Ala Asn Val Met Lys Thr Leu Gln His Glu
 275 280 285

Arg Leu Val Arg Leu Tyr Ala Val Val Thr Arg Glu Pro Ile Tyr Ile
 290 295 300

Val Thr Glu Tyr Met Ala Arg Gly Cys Leu Leu Asp Phe Leu Lys Thr
 305 310 315 320

41

Asp Glu Gly Ser Arg Leu Ser Leu Pro Arg Leu Ile Asp Met Ser Ala
 325 330 335
 Gln Val Ala Glu Gly Met Ala Tyr Ile Glu Arg Met Asn Ser Ile His
 340 345 350
 Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Ser Glu Thr Leu Cys Cys
 355 360 365
 Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile Ile Asp Ser Glu Tyr Thr
 370 375 380
 Ala Gln Glu Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala
 385 390 395 400
 Ile His Phe Gly Val Phe Thr Ile Lys Ala Asp Val Trp Ser Phe Gly
 405 410 415
 Val Leu Leu Met Val Ile Val Thr Tyr Gly Arg Val Pro Tyr Pro Gly
 420 425 430
 Met Ser Asn Pro Glu Val Ile Arg Ser Leu Glu His Gly Tyr Arg Met
 435 440 445
 Pro Cys Pro Glu Thr Cys Pro Pro Glu Leu Tyr Asn Asp Ile Ile Thr
 450 455 460
 Glu Cys Trp Arg Gly Arg Pro Glu Glu Arg Pro Thr Phe Glu Phe Leu
 465 470 475 480
 Gln Ser Val Leu Glu Asp Phe Tyr Thr Ala Thr Glu Gly Gln Tyr Glu
 485 490 495
 Leu Gln Pro

<210> 20

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<221> modified_base

<222> (14)

<223> A, T, C, G, other or unknown

<220>

<221> modified_base

<222> (20)

<223> A, T, C, G, other or unknown

<220>

<221> modified_base

<222> (23)

<223> A, T, C, G, other or unknown

<220>

<221> modified_base

42

<222> (26)

<223> A, T, C, G, other or unknown

<220>

<223> Description of Artificial Sequence: Primer

<400> 20

ggaattccca ymgnrayytn rcnrcnmg

28

<210> 21

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<221> modified_base

<222> (12)

<223> A, T, C, G, other or unknown

<220>

<221> modified_base

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<220>

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<220>

<223> Description of Artificial Sequence: Primer

<400> 21

ggaattccrw rnswwcanac stcnsa

26

<210> 22

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 22

Gly	Gln	Asp	Ala	Asp	Gly	Ser	Thr	Ser	Pro	Arg	Ser	Gln	Glu	Pro
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<210> 23

<211> 16

<212> PRT

<213> Artificial Sequence

43

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 23

Gln	Gln	Leu	Leu	Ser	Ser	Ile	Glu	Pro	Leu	Arg	Glu	Lys	Asp	Lys	His
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<210> 24

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative
peptide

<220>

<221> MOD_RES

<222> (6)

<223> Variable amino acid

<400> 24

Ser	Asp	Val	Trp	Ser	Xaa
1				5	